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Comparative Genomics of Darren, BillyBob and MrBubbles

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Our SEA PHAGES course completed short comparative genomics projects to understand more about phages discovered by our classmates. The comparison of bacteriophage genomes allows us to better understand viral evolution. By comparing certain defining characteristics and traits of a genome, areas of similarity and differences can be uncovered to give more information regarding the history and evolutionary relationships between the genomes. Our projects focused on comparing whole genomes of phages Darren, BillyBob and MrBubbles, as well as gene families including proteins from these phages. Darren is 160,916 base pairs long, has a 2,585 base bair long terminal repeat and a 38.7% GC content. There are 292 predicted open reading frames. BillyBob is a bacteriophage with a 165,429 base pair genome with a terminal repeat of 2,262 base pairs. It is 37.2% GC content with 294 predicted open reading frames. MrBubbles is 161,581 base pairs long with a 2,584 base pair long terminal repeat, a GC content of 38.2% and 291 predicted open reading frames. Blastn was used to determine best matches to each of these phages in Genbank. Multiple programs were used to compare protein sequences, visualize phylogeny and map out the genes within each genome. These results are in progress and will be presented to compare and contrast these three genomes with each other and with ‘relatives’ from the Bacillus Phage Database.